

SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Goli, Surya K.
Hillman, Jennifer L.
Murry, Lynn E.
 - (ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID
RECEPTOR PROTEIN
 - (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0233 US
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: CONUTUT01

(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Ala	Glu	Asp	Val	Val	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Asp	Leu
1				5					10					15	
Glu	Ser	Gly	Gly	Leu	Leu	His	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu
		20						25					30		
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly
		35					40					45			
Asp	Gln	Pro	Ala	Ala	Ser	Gly	Asp	Arg	Thr	Thr	Thr	Xaa	Pro	Pro	Pro
	50					55					60				
Leu	Pro	Arg	Leu	Lys	Arg	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg
65				70					75					80	
Phe	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys
			85					90					95		
Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro
			100					105					110		
Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe
	115					120						125			
Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp
	130					135					140				
Leu	Thr	Ala	Ala	Gln	Gln	Glu	Thr	Leu	Ser	Asp	Trp	Glu	Ser	Gln	Phe
145				150					155					160	
Thr	Phe	Lys	Tyr	His	His	Val	Gly	Lys	Leu	Leu	Lys	Glu	Gly	Glu	Glu
			165					170						175	
Pro	Thr	Val	Tyr	Ser	Asp	Glu	Glu	Glu	Pro	Lys	Asp	Glu	Ser	Ser	Arg
			180					185					190		
Lys	Asn	Val	Lys	Ala	Phe	Ser	Gly	Ser	Ile	Ser	Xaa	Xaa	Tyr	Phe	Ala
	195						200					205			
Lys	Ser	Phe	Val	Thr	Val	His	Xaa	Val	Phe	Lys	Thr				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01
- (B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCGCCGAAC	CCCGCGCGCC	ACTCGCTCGC	TCAGAGGGAG	GAGAAAGTGG	CGAGTTCCGG	60
ATCCCTGCCT	AGCGCGGCCC	AACCTTTACT	CCAGAGATCA	TGGCTGCCGA	GGATGTGGTG	120
GCGACTGGCG	CCGACCCAAG	CGATCTGGAG	AGCGGCGGGC	TGCTGCATGA	GATTTTCACG	180
TCGCCGCTCA	ACCTGCTGCT	GCTTGGCCTC	TGCATCTTCC	TGCTCTACAA	GATCGTGCGC	240
GGGGACCAGC	CGGCGGCCAG	CGGCGACAGG	ACGACGACGA	NGCCGCCCCC	TCTGCCCCGC	300
CTCAAGCGGC	GCGACTTCAC	CCCCGCCGAG	CTGCGGCGCT	TCGACGGCGT	CCAGGACCCG	360
CGCATACTCA	TGGCCATCAA	CGGCAAGGTG	TTCGATGTGA	CCAAAGGCCG	CAAATTCTAC	420
GGGCCCCGAGG	GGCCGTATGG	GGTCTTTGCT	GGAAGAGATG	CATCCAGGGG	CCTTGCCACA	480
TTTTGCCTGG	ATAAGGAAGC	ACTGAAGGAT	GAGTACGATG	ACCTTTCTGA	CCTCACTGCT	540
GCCCCAGCAGG	AGACTCTGAG	TGACTGGGAG	TCTCAGTTCA	CTTTCAAGTA	TCATCACGTG	600
GGCAAAGTGC	TGAAGGAGGG	GGAGGAGCCC	ACTGTGTACT	CAGATGAGGA	AGAACCAAAA	660
GATGAGAGTT	CCCGGAAAAA	TGTTAAAGCA	TTCAGTGGA	GTATATCTAT	NNTGATTTTT	720

GCAAAATCAT TTGTAACAGT CCACTNTGTC TTAAACAT AGTGTTACAA TATTTAGAAA 780
 GTTTGAGC 788

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1518818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Ala	Glu	Asp	Val	Val	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Glu	Leu	1	5	10	15
Glu	Gly	Gly	Gly	Leu	Leu	Gln	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu	20	25	30	
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly	35	40	45	
Asp	Gln	Pro	Gly	Ala	Ser	Gly	Asp	Asn	Asp	Asp	Asp	Glu	Pro	Pro	Pro	50	55	60	
Leu	Pro	Arg	Leu	Lys	Pro	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg	65	70	75	80
Tyr	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys	85	90	95	
Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro	100	105	110	
Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe	115	120	125	
Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp	130	135	140	
Leu	Thr	Pro	Ala	Gln	Gln	Glu	Thr	Leu	Asn	Asp	Trp	Asp	Ser	Gln	Phe	145	150	155	160
Ser	Ser	Pro	Ser	Ser	Thr	Ile	Thr	Trp	Gly	Lys	Leu	Leu	Glu	Gly	Ala	165	170	175	
Glu	Glu	Pro	Ile	Val	Tyr	Ser	Asp	Asp	Glu	Glu	Gln	Lys	Met	Arg	Leu	180	185	190	
Leu	Gly	Arg	Val	Thr	Glu	Ala	Val	Ser	Gly	Ala	Tyr	Leu	Phe	Leu	Tyr	195	200	205	
Phe	Ala	Lys	Ser	Phe	Val	Thr	Phe	Gln	Ser	Val	Phe	Thr	Thr	Trp		210	215	220	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1657409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

PF-0233-2 CON

Met	Ala	Ala	Glu	Asp	Val	Ala	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Glu	Leu	1	5	10	15
Glu	Gly	Gly	Gly	Leu	Leu	His	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu	20	25	30	
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly	35	40	45	
Asp	Gln	Pro	Ala	Ala	Ser	Asp	Ser	Asp	Asp	Asp	Glu	Pro	Pro	Pro	Leu	50	55	60	
Pro	Arg	Leu	Lys	Arg	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg	Phe	65	70	75	80
Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys	Val	85	90	95	
Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro	Tyr	100	105	110	
Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe	Cys	115	120	125	
Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp	Leu	130	135	140	
Thr	Pro	Ala	Gln	Gln	Glu	Thr	Leu	Asn	Asp	Trp	Asp	Ser	Gln	Phe	Thr	145	150	155	160
Phe	Lys	Tyr	His	His	Val	Gly	Lys	Leu	Leu	Lys	Glu	Gly	Glu	Glu	Pro	165	170	175	
Thr	Val	Tyr	Ser	Asp	Glu	Glu	Glu	Pro	Lys	Asp	Glu	Ser	Ala	Arg	Lys	180	185	190	
Asn	Asp																		